

CGCAATTAGAAATGCTCTCGCAAGCCGTCGTGTAGGAGACGGGTTCGGAGC

A L I F T M A F G S T S S A Q A S

100

FIG. 2A

A L I F T M A F G S T S S A Q A S
 GCGTTAATCTTTACGATGGCGTTCGGCAGCACATCCTCTGCCCAAGCCTCG

3' NNNNNNNNN

124

102

A

T

T

A

A

T

C

A

T

C

T

T

C

G

A

A

T

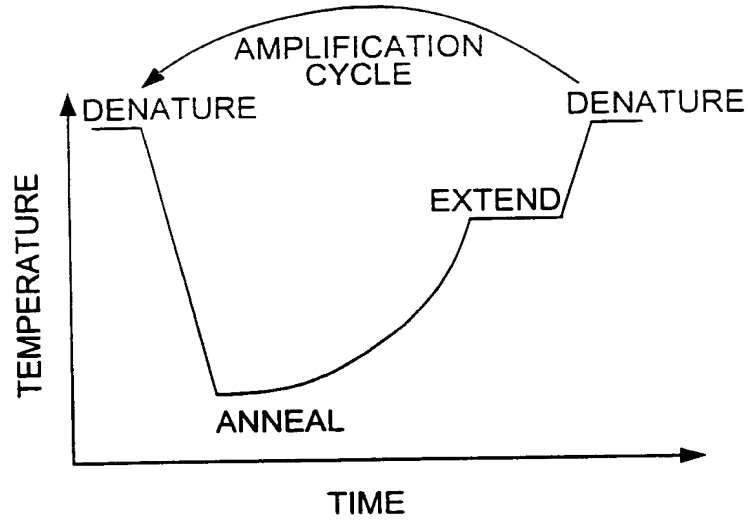
A

5'

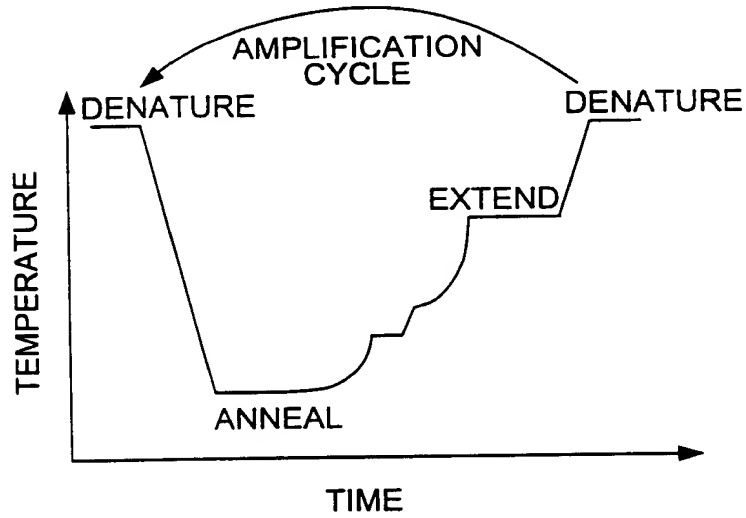
120

FIG. 2B

A



B



C

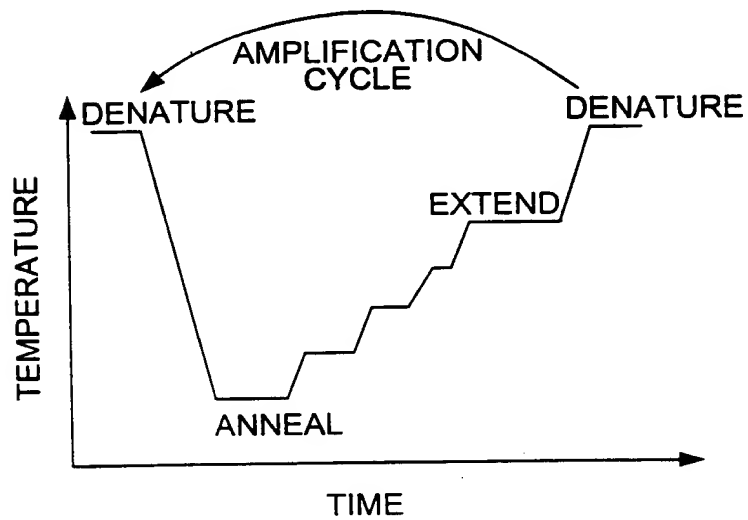


FIG. 3

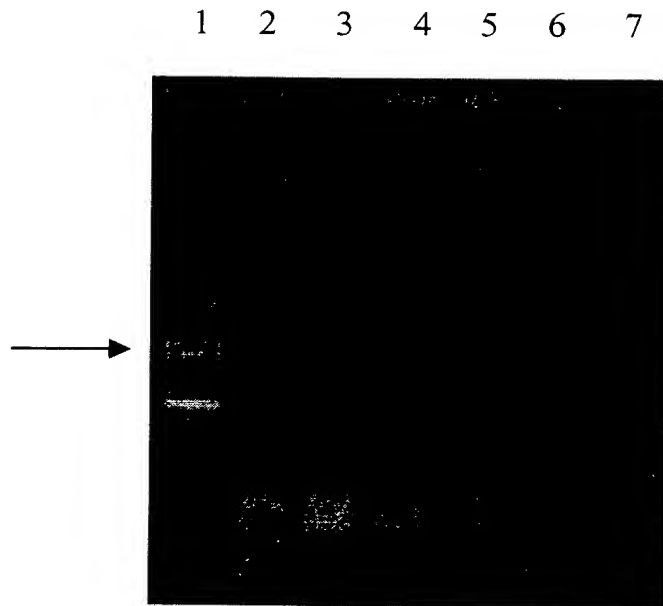


FIGURE 4

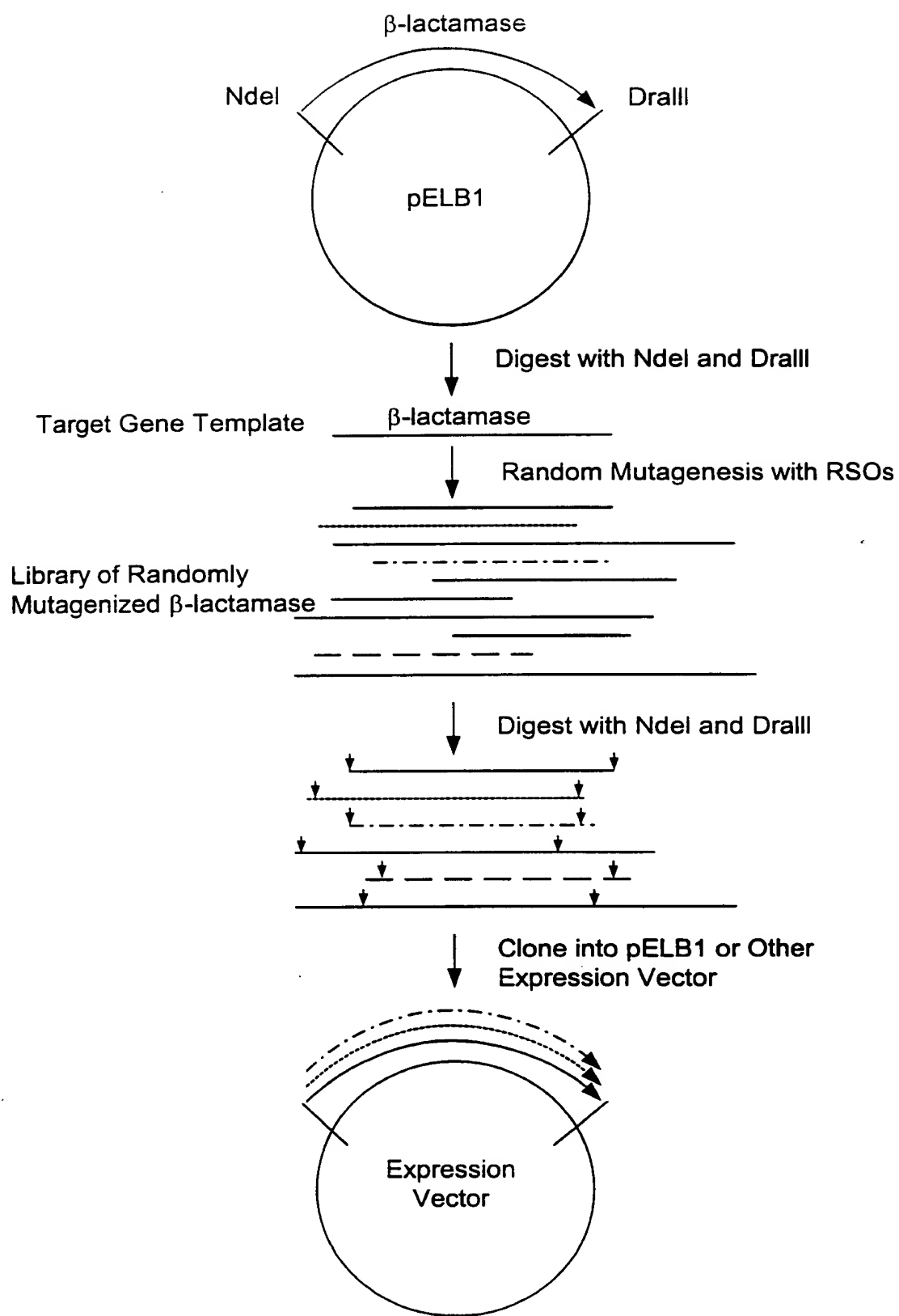


FIG. 5